SEQUENCE LISTING

- (1) GENERAL INFORMATION:
 - (i) APPLICANT:

(countries other than US) AMRAD OPERATIONS PTY. LTD. (us only) Hayward, N and Weber, G

- (ii) TITLE OF INVENTION: A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING SAME
- (iii) NUMBER OF\SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: DAVIES COLLISON CAVE
 - (B) STREET: 1 LYTTLE COLLINS STREET
 - (C) CITY: MELBOURNE
 - (D) STATE: VICTORIA
 - (E) COUNTRY: AU\$TRALIA
 - (F) ZIP: 3000
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn\Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT INTERNATIONAL
 - (B) FILING DATE: 22-FEB-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: AU PN1457
 - (B) FILING DATE: 02-MAR-1995
 - (A) APPLICATION NUMBER: AU PN6647
 - (B) FILING DATE: 20-NOV-1995
 - (A) APPLICATION NUMBER: AU \PN7274
 - (B) FILING DATE: 22-DEC-1995

(viii) ATTORNEY/AGENT INFORMATION:	
(A) NAME: HUGHES DR, E JOHN L	
(C) REFERENCE/DOCKET NUMBER: EJH/EK	
(ix) TELECOMMUNICATION INFORMATION:	
(A) TELEPHONE: +61 3 9254 2777	
(B) TELEFAX: +61 3 9254 2770	
(2) INFORMATION FOR SEQ ID NO:1:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 649 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA	-
,,	
(ix) FEATURE: (A) NAME/KEY: CDS	
(B) LOCATION: 17\589	
()	
(xi) SEQUENCE DESCRIPTION SEQ ID NO:1:	
\	4.5
TCGGGCCTCC GAAACC ATG AAC TTT CTG CTG TCT TGG GTG CAT TGG AGC Met Asn Phe Leu Leu Ser Trp Val His Trp Ser	49
1 5 10	
CTT GCC TTG CTG CTC TAC CTC CAC CAT GCC AAG TGG TCC CAG GCT GCA	97
Leu Ala Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala	
15 20 25	
CCC ATG GCA GAA GGA GGG CAG AAT CAC GAA GTG GTG AAG TTC	145
Pro Met Ala Glu Gly Gly Gln Asn His His Glu Val Val Lys Phe	
30 35 \ 40	
ATG GAT GTC TAT CAG CGC AGC TAC TGC CAT CCA ATC GAG ACC CTG GTG	193
Met Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val	
45 50 \ 55	
GAC ATC TTC CAG GAG TAC CCT GAT GAG ATC GAG TAC ATC TTC AAG CCA	241
Asp Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro 60 65 70 75	
TCC TGT GTG CCC CTG ATG CGA TGC GGG GGC TGC TGC AAT GAC GAG GGC Ser Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly	289
set che sat eto pen uer wid che ath ath che che wen web ath ath	



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CTG Leu	GAG Glu	TGT Cys	GTG Val 95	ccc Pro	ACT Thr	GAG Glu	GAG Glu	TCC / Ser 100	AAC A Asn	ATC A Ile	CC A	TG C. Met	AG A Gln 105	TT AT	rg Met	337
CGG Arg	ATC Ile	AAA Lys 110	CCT Pro	CAC His	CAA Gln	GGC Gly	CAG Gln 115	CAC I	ATA G	GA G Gly	AG A' Glu	TG A Met 120	GC T Ser	rc Cl Phe	rA Leu	385
CAG Gln	CAC His 125	AAC Asn	AAA Lys	TGT Cys	GAA Glu	TGC . Cys \130	AGA (Arg	CCA I Pro	AAG A Lys	AA G Lys	AT AG Asp 7	GA GO Arg	CA AC	GA CA Arg	A Gln	433
GAA Glu 140	AAT Asn	CCC Pro	TGT Cys	GGG Gly	CCT Pro 145	cha 180	TCA (Ser	GAG (GG A Arg	GA A Arg 150	AG CA	AT T His	rg Ti Leu	Phe '	TA Val 155	481
CAA Gln	GAT Asp	CCG Pro	CAG Gln	ACG Thr 160	TGT Cys	AAA Lys	Cys	TCC I Ser	Cys 165	AA A Lys	AC A(Asn '	CA GI	Asp	CG CG Ser 7	IT Arg	529
TGC Cys	AAG Lys	GCG Ala	AGG Arg 175	CAG Gln	CTT Leu	GAG :	Leu	AAC G Asn 180	Glu	GT A Arg	CT TO Thr (Cys	GA TO Arg 185	GT GA Cys /	LC As p	577
		AGG Arg 190		TGAG	CCGG	GC A	GGAG	GAAGG	G AGO	CTCC	CTC .	AGCG	TTTC	GG		629
GAAC	CAGA	ATC T	CTCA	CCAC	₽ G											649
(2)	INFO	RMA	rion	FOR	SEQ	ID N	TO:2	:	\							
		(i) \$	(A) (B)	LEI TYI	NGTH PE: 8		am:									
	(i	Li) N	MOLEC	TULE	TYP	E: pı	rote:	in		/	\·					
	()	ci) S	SEQUI	ENCE	DES	CRIP:	rion	: SE(O ID	NO: 2						
Met 1	Asn	Phe	Leu	Leu 5	Ser	Trp	Val	His	Trp 10	Ser	Leu	Ala	Leu	Leu 15	Leu	
Tyr	Leu	His	His 20	Ala	Lys	Trp	Ser	Gln 25	Ala	Ala	Pro	Met	Ala 30	Glu	Gly	
		35					40				Met	45\	\			
Arg	Ser 50	Tyr	Сув	His	Pro	Ile 55	Glu	Thr	Leu	Val	Asp 60	Ile	Phe	Gln	Glu	

Aut 3

- 39 -

	Asp	Glu	Ile	Glu 70	Tyr	Ile	Phe	Lys	Pro 75	Ser	Cys	Val	Pro	Let 80
Arg	Cys	dis	Gly 85	Cys	Cys	Asn	Asp	Glu 90	Gly	Leu	Glu	Cys	Val 95	Pro
Glu	Glu	Sex 100	Asn	Ile	Thr	Met	Gln 105	Ile	Met	Arg	Ile	Lys 110	Pro	His
Gly	Gln 115	His	le	Gly	Glu	Met 120	Ser	Phe	Leu	Gln	His 125	Asn	Lys	Суз
Cys 130	Arg	Pro	Lya	Lys \	Asp 135	Arg	Ala	Arg	Gln	Glu 140	Asn	Pro	Cys	Gly
Cys	Ser	Glu	Arg	Arg 150	Lys	His	Leu	Phe	Val 155	Gln	Asp	Pro	Gln	Thr 160
Lys	Cys	Ser	Cys 165	Lys	Asn	Thr	Asp	Ser 170	Arg	Cys	Lys	Ala	Arg 175	Glr
Glu	Leu	Asn 180	Glu	Arg	The	Cys	Arg 185	Cys	Asp	Lys	Pro	Arg 190	Arg	
	Arg Glu Gly Cys 130 Cys	Arg Cys Glu Glu Gly Gln 115 Cys Arg 130 Cys Ser Lys Cys	Arg Cys Gly Glu Glu Ser 100 Gly Gln His 115 Cys Arg Pro 130 Cys Ser Glu Lys Cys Ser Glu Leu Asn	Arg Cys Gly Gly 85 Glu Glu Ser Asn 1000 Gly Gln His 1le 115 Cys Arg Pro Lys 130 Cys Ser Glu Arg Lys Cys Ser Cys 165 Glu Leu Asn Glu	Arg Cys Gly Gly Cys 85 Glu Glu Ser Asn Ile 100 Gly Gln His Ile Gly 115 Cys Arg Pro Lys Lys 130 Cys Ser Glu Arg Arg 150 Lys Cys Ser Cys Lys 165 Glu Leu Asn Glu Arg	Arg Cys Gly Gly Cys Cys 85 Glu Glu Ser Asn Ile Thr 100 Gly Gln His Ile Gly Glu 115 Cys Arg Pro Lys Lys Asp 130 Cys Ser Glu Arg Arg Lys 150 Lys Cys Ser Cys Lys Asn 165 Glu Leu Asn Glu Arg Thr	Arg Cys Gly Gly Cys Cys Asn Slu Glu Glu Ser Asn Ile Thr Met 100 Gly Glu Met 120 Cys Arg Pro Lys Lys Asp Arg 130 Cys Ser Glu Arg Arg Lys His 150 Cys Cys Ser Cys Lys Asn Thr 165 Cys Thr Cys	Arg Cys Gly Gly Cys Cys Asn Asp 85 Glu Glu Ser Asn Ile Thr Met Gln 105 Gly Gln His Ile Gly Glu Met Ser 120 Cys Arg Pro Lys Lys Asp Arg Ala 135 Cys Ser Glu Arg Arg Lys His Leu 150 Lys Cys Ser Cys Lys Asn Thr Asp 165 Glu Leu Asn Glu Arg Thr Cys Arg	Arg Cys Gly Gly Cys Cys Asn Asp Glu 85 Cys Glu Asn Asp Glu 90 Glu Glu Ser Asn Ile Thr Met Gln Ile 105 Gly Gln His Ile Gly Glu Met Ser Phe 120 Cys Arg Pro Lys Lys Asp Arg Ala Arg 135 Cys Ser Glu Arg Arg Lys His Leu Phe 150 Lys Cys Ser Cys Lys Asn Thr Asp Ser 165 Glu Leu Asn Glu Arg Thr Cys Arg Cys	Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Glu Glu Glu Ser Asn Ile Thr Met Gln Ile Met 105 Gly Gln His Ile Gly Glu Met Ser Phe Leu 120 Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln 130 Cys Ser Glu Arg Arg Lys His Leu Phe Val 150 Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg 170 Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp	Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu 85 Cys Asn Asp Glu Gly Leu 90 Glu	Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile 100 Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His 115 Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn 130 Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp 150 Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys 165 Thr Cys Arg Cys Asp Lys Pro	Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys 90 Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys 110 Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn 125 Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro 130 Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro 155 Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg	Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val 95 Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro 100 Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys 125 Cys Arg Pro Lya Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys 130 Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln 155 Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg 175 Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg Arg Arg Arg Cys Arg Arg Arg Arg Arg Arg Arg Arg Arg Cys Arg

- (2) INFORMATION FOR SEQ ID NO:\3:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1094 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 3..624
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO 3:
- CC ATG AGC CCT CTG CTC CGC CGC CTG CTG CTC CCC GCA CTC CTG CAG

 Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln

 1 5 10 15
- CTG GCC CCC GCC CAG GCC CCT GTC TCC CAG CCT GAT GCC CCT GGC CAC

 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His

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- CAG AGG AAA GTG GTG TCA TGG ATA GAT GTG TAT ACT CGC GCT ACC TGC

 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys

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CAG CCC CGG GAG GTG GTG CCC TTG ACT GTG GAG CTC ATG GGC ACC 191 Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr 50 GTG GCC AAA CAG\CTG GTG CCC AGC TGC GTG ACT GTG CAG CGC TGT GGT 239 Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly GGC TGC TGC CCT GAQ GAT GGC CTG GAG TGT GTG CCC ACT GGG CAG CAC 287 Gly Cys Cys Pro Asp\ Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His 85 335 CAA GTC CGG ATG CAG ATC CTC ATG ATC CGG TAC CCG AGC AGT CAG CTG Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu 105 100 GGG GAG ATG TCC CTG GAA GAA CAC AGC CAG TGT GAA TGC AGA CCT AAA 383 Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys 115 120 AAA AAG GAC AGT GCT GTG AAG CCA GAC AGG GCT GCC ACT CCC CAC CAC 431 Lys Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His 130 13 479 CGT CCC CAG CCC CGT TCT GTT CCG GCC TGG GAC TCT GCC CCC GGA GCA Arg Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala 150 527 CCC TCC CCA GCT GAC ATC ACC CAT CCC ACT CCA GCC CCA GGC CCC TCT Pro Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser 170 165 GCC CAC GCT GCA CCC AGC ACC AGC GCC\CTG ACC CCC GGA CCT GCC 575 Ala His Ala Ala Pro Ser Thr Thr Ser Ala\Leu Thr Pro Gly Pro Ala 185 180 GCT GCC GCT GCC GAC GCC GCA GCT TCC TCC GTT GCC AAG GGC GGG GCT T 624 Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala 205 200 195 AGAGCTCAAC CCAGACACCT GCAGGTGCCG GAAGCTGCGA AGGTGACACA TGGCTTTTCA 684 GACTCAGCAG GGTGACTTGC CTCAGAGGCT ATATCCCAGT GGGGGAACAA AGGGGAGCCT 744 GGTAAAAAAC AGCCAAGCCC CCAAGACCTC AGCCCAGGCA GAAGQTGCTC TAGGACCTGG 804 GCCTCTCAGA GGGCTCTTCT GCCATCCCTT GTCTCCCTGA GGCCATCATC AAACAGGACA 864 GAGTTGGAAG AGGAGACTGG GAGGCAGCAA GAGGGGTCAC ATACCAGQTC AGGGGAGAAT 924 GGAGTACTGT CTCAGTTTCT AACCACTCTG TGCAAGTAAG CATCTTACAA CTGGCTCTTC 984 CTCCCCTCAC TAAGAAGACC CAAACCTCTG CATAATGGGA TTTGGGCTTT GGTACAAGAA 1044 1094



(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
- (B) TYPE: amino acid
- (N) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln

Arg Lys Val Val Ser Trp tle Asp Val Tyr Thr Arg Ala Thr Cys Gln

Pro Arg Glu Val Val Pro\Leu Thr Val Glu Leu Met Gly Thr Val

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly 65

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln

Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly

Glu Met Ser Leu Glu Glu His Ser Gln dys Glu Cys Arg Pro Lys Lys 115 120

Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Thr Pro His His Arg

Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro

Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala\Pro Gly Pro Ser Ala 165

His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala Ala 185

Ala Ala Ala Asp Ala Ala Ser Ser Val Ala Lys\Gly Gly Ala 200 \205 195

(2) INFORMATION FOR SEQ ID NO:5:	
(i) SEQUENÇE CHARACTERISTICS:	
(A) LENGTH: 993 base pairs	
(B) TYRE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA	
(ix) FEATURE:	
(A) NAME/KEY: CDS	
(B) LOCATION 3566	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
CC ATG AGC CCT CTG CTC CGC CGC CTG CTG CTC GCC GC	47
Met Ser Pro Leu Leu Arg\Arg Leu Leu Leu Ala Ala Leu Leu Gln	
1 5 \ 10 15	
CTG GCC CCC GCC CAG GCC CCT GTC TCC CAG CCT GAT GCC CCT GGC CAC	95
Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His	
20 25 30	
CAG AGG AAA GTG GTG TCA TGG ATA GAT GTG TAT ACT CGC GCT ACC TGC	143
Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys	
35 40 45	
CAG CCC CGG GAG GTG GTG CCC TTG ACT GTG GAG CTC ATG GGC ACC	191
Gln Pro Arg Glu Val Val Pro Leu Thr Val Glu Leu Met Gly Thr	
50 55 \ 60	
THE SECOND SECON	239
GTG GCC AAA CAG CTG GTG CCC AGC TGC GTG ACT GTG CAG CGC TGT GGT Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly	233
65 70 75	
GGC TGC TGC CCT GAC GAT GGC CTG GAG TGT GTG CCC ACT GGG CAG CAC	287
Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His	
80 85 99	
CAA GTC CGG ATG CAG ATC CTC ATG ATC CGG TAC CCG AGC AGT CAG CTG	335
Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu	
100 105 \ 110	
	202
GGG GAG ATG TCC CTG GAA GAA CAC AGC CAG TGT GAA TGC AGA CCT AAA Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys	383
115 120 Let GIU GIU HIS SET GIT CYS GIU CYS AIG FIO DYS	
\ ===	
AAA AAG GAC AGT GCT GTG AAG CCA GAT AGC CCC AGG CCC CTC TGC CCA	431
Lys Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro	
130 135 149	

July Charles



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CGC TGC ACC CAG CAC CAG CGC CCT GAC CCC CGG ACC TGC CGC TGC Arg Cys Thr Gln Ais His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys 145 150 155	479
CGC TGC CGA CGC CGC AGC TTC CTC CGT TGC CAA GGG CGG GGC TTA GAG Arg Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu 160 175	527
CTC AAC CCA GAC ACC TGC AGG TGC CGG AAG CTG CGA AGG TGACACATGG Leu Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg 180 185	576
CTTTTCAGAC TCAGCAGGGT GACTTGCCTC AGAGGCTATA TCCCAGTGGG GGAACAAAGG	636
GGAGCCTGGT AAAAAACAGC CAAGCCCCCA AGACCTCAGC CCAGGCAGAA GCTGCTCTAG	696
SACCTGGGCC TCTCAGAGGG CTCTTCTGCC ATCCCTTGTC TCCCTGAGGC CATCATCAAA	756
CAGGACAGAG TTGGAAGAGG AGACTGGGAG GCAGCAAGAG GGGTCACATA CCAGCTCAGG	816
GAGAATGGA GTACTGTCTC AGTTTCTAAC CACTCTGTGC AAGTAAGCAT CTTACAACTG	876
SCTCTTCCTC CCCTCACTAA GAAGACCCAA ACCTCTGCAT AATGGGATTT GGGCTTTGGT	936
ACAAGAACTG TGACCCCCAA CCCTGATAAA AGAGATGGAA GGAAAAAAAA AAAAAAA	993
(2) INFORMATION FOR SEO ID NO:6 \	

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 188 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ TD NO:6:

Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln 20

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly 75 65 70

Cys	Cys	Pro	Asp	Asp 85	Gly	Leu	Glu	Cys	Val 90	Pro	Thr	Gly	Gln	His 95	Gln	
Val	Arg	Met	Gln 100	1	Leu	Met	Ile	Arg 105	Tyr	Pro	Ser	Ser	Gln 110	Leu	Gly	
Glu	Met	Ser 115	Leu	Glu	Glu	His	Ser 120	Gln	Cys	Glu	Cys	Arg 125	Pro	Lys	Lys	
Lys	Asp 130	Ser	Ala	Val	Lys	Pro 135	Asp	Ser	Pro	Arg	Pro 140	Leu	Cys	Pro	Arg	
Cys 145	Thr	Gln	His	His	G)n 150	Arg	Pro	Asp	Pro	Arg 155	Thr	Cys	Arg	Cys	Arg 160	
Cys	Arg	Arg	Arg	Ser 165	Phe	Leu	Arg	Cys	Gln 170	Gly	Arg	Gly	Leu	Glu 175	Leu	
Asn	Pro	Asp	Thr 180	Cys	Arg	Cys	Arg	Lys 185	Leu	Arg	Arg					
						'	\									
(2)	INFC	RMAT	NOI	FOR	SEQ	ID N	7 / 10									
	(i)	(A (B	L) LE L) TY	NGTH PE: RAND	IARAC I: 85 nucl EDNE	8 ba eic SS:	se p acid sing	airs	3							
	(ii)	MOL	ECUL	E TY	PE:	DNA		\								
	(ix)		AN (ME/K	EY:		31									
	(xi)	SEQ	UENC	E DE	SCRI	PTIO	N: S	EQ I	ои о	:7:						
CC A					TC Co eu A 5											47
CTG (95
Leu 2	ата	PTO	Ala	GIN	ΑΙα	Pro	vaı	ser	GID	PTO	ASP	ALA	PLO	GTÄ	nls	

CAG AGG AAA GTG GTG TCA TGG ATA GAT GTG TAT ACT COC GCT ACC TGC Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys

CAG CCC CGG GAG GTG GTG CCC TTG ACT GTG GAG CTC ATG GGC ACC

Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr

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191

' \	
GTG GCC AAA CAG CTG GTG CCC AGC TGC GTG ACT GTG CAG CGC TGT GGT Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Ary Cys Gly 65 70 75	239
GGC TGC TGC CCT GAC GAT GGC CTG GAG TGT GTG CCC ACT GGG CAG CAC Gly Cys Cys Pro Asb Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His 80 90 95	287
CAA GTC CGG ATG CAG ATC CTC ATG ATC CGG TAC CCG AGC AGT CAG CTG Gln Val Arg Met Gln Ite Leu Met Ite Arg Tyr Pro Ser Ser Gln Leu 100 105 110	335
GGG GAG ATG TCC CTG GAA GAA CAC AGC CAG TGT GAA TGC AGA CCT AAA Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys 115 120 125	383
AAA AAG GAC AGT GCT GTG AAG CCA GAT AGG TGC CGG AAG CTG CGA AGG Lys Lys Asp Ser Ala Val Lys Pro Asp Arg Cys Arg Lys Leu Arg Arg 130 140	431
TGACACATGG CTTTTCAGAC TCAGCAGGGT GACTTGCCTC AGAGGCTATA TCCCAGTGGG	491
GGAACAAAGG GGAGCCTGGT AAAAAACAGC CAAGCCCCCA AGACCTCAGC CCAGGCAGAA	551
GCTGCTCTAG GACCTGGGCC TCTCAGAGGG CTCTTCTGCC ATCCCTTGTC TCCCTGAGGC	611
CATCATCAAA CAGGACAGAG TTGGAAGAGG AGACTGGGAG GCAGCAAGAG GGGTCACATA	671
CCAGCTCAGG GGAGAATGGA GTACTGTCTC AGTTTCTAAC CACTCTGTGC AAGTAAGCAT	731
CTTACAACTG GCTCTTCCTC CCCTCACTAA GAAGACCCAA ACCTCTGCAT AATGGGATTT	791
GGGCTTTGGT ACAAGAACTG TGACCCCCAA CCCTGATAAA AGAGATGGAA GGAAAAAAAA	851
АААААА	858

- (2) INFORMATION FOR SEQ ID NO:8:
 - (i) SEQUENCE CHARACTERISTICS:
 - (À) LENGTH: 143 amino acids
 - (B) TYPE: amino acid
 - (D) \TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
1 5 10 15

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
20 25 30

Arg Lys Val Val Ser Trp tle Asp Val Tyr Thr Arg Ala Thr Cys Gln
35 40 45

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
50 55 60

Ala Lys Gln Leu Val Pro Ser dys Val Thr Val Gln Arg Cys Gly Gly 65 70 75 80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
85 90 95

Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
100 105 110

Glu Met Ser Leu Glu Glu His Ser Gla Cys Glu Cys Arg Pro Lys Lys

Lys Asp Ser Ala Val Lys Pro Asp Arg Cys Arg Lys Leu Arg Arg
130 135 140

455

515

575

635

695

(2)	INFORMATION	FOR	SEQ	ID	NO:9:

	1	
/: \	CECTIONICE	CHARACTERISTICS:

- (A) LENGTH: 910 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (ix) FEATURE:
 - (A) NAME KEY: CDS

100

- (B) LOCATION: 3..305
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

\	
CC ATG AGC CCT CTG CTC CGC CGC CTG CTG CTC GCC GC	
1 5 10 10 10	
CTG GCC CCC GCC CAG GCC CCT GTC TCC CAG CCT GAT GCC CCT GGC CA Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly H:	
CAG AGG AAA GTG GTG TCA TGG ATA GAT GTG TAT ACT CGC GCT ACC TGC	143
Gln Arg Lys Val Val Ser Trp tle Asp Val Tyr Thr Arg Ala Thr Cy 35 40 45	ys
CAG CCC CGG GAG GTG GTG GTG CCC TTG ACT GTG GAG CTC ATG GGC ACC	191
Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Th	hr
GTG GCC AAA CAG CTG GTG CCC AGC TGC GTG ACT GTG CAG CGC TGT GGT	239
Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys G	ly
65 70 75	
GGC TGC TGC CCT GAC GAT GGC CTG GAG TGT GTG CCC ACT GGG CAG CAC	
Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln H	
80 85 90	95
CAA GTC CGG ATG CAG ACC TAAAAAAAAG GACAGTGCTG TGAAGCCAGA	335
Gln Val Arg Met Gln Thr	

CAGGGCTGCC ACTCCCCACC ACCGTCCCCA GCCCCGTCT GTTCCGGGCT GGGACTCTGC

CCCCGGAGCA CCCTCCCCAG CTGACATCAC CCATCCCACT CCAGCCCCAG GCCCCTCTGC

CCACGCTGCA CCCAGCACCA CCAGCGCCCT GACCCCCGGA\CCTGCCGCTG CCGCTGCCGA

CGCCGCAGCT TCCTCCGTTG CCAAGGGCGG GGCTTAGAGC TCAACCCAGA CACCTGCAGG

TGCCGGAAGC TGCGAAGGTG ACACATGGCT TTTCAGACTC AGCAGGGTGA CTTGCCTCAG

AGGCTATATC CCAGTGGGGA ACAAAGAGGA GCCTGGTAAA AAA\AGCCAA GCCCCCAAGA

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CCTCAGCCCA	GGCAGAAGCT	GCTCTAGGAC	CTGGGCCTCT	CAGAGGGCTC	TTCTGCCATC	75
CCTTGTCTCC	CTGAGCCAT	CATCAAACAG	GACAGAGTTG	GAAGAGGAGA	CTGGGAGGCA	819
GCAAGAGGGG	TCACATACCA	GCTCAGGGGA	GAATGGAGTA	CTGTCTCAGT	TTCTAACCAC	879
TCTGTGCAAG	TAAGCATCTT	ACAACTGGCT	CTTCC			910

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 101 amino acids
 - (B) TYPE: \amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
1 5 10 15

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
20 25 30

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
35 45

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val

. 50 55 60

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
65 70 75 80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln 85 90 95

Val Arg Met Gln Thr 100

(2) INFORMATION FOR SEQ ID NO:11:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(b) IDFOLOGI. 12Med1
(ii) MOLECULE TYPE: Oligonucleotide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
ACCACCACCT CCCTGGGCTG GCATGTGGCA CGTGCATAAA CG 4
(2) INFORMATION FOR SEQ ID NO:12:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE:\Oligonucleotide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
AGTTGTTTGA CCACATTGCC CATGAGTTCC ATGCTCAGAG GC 4
(2) INFORMATION FOR SEQ ID NO:13:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Oligonucleotide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
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GATCCTGGGG CTGGAGTGGG ATGGATGATG TCAGCTGG

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCGGGCAGAG GATCCTGGGG CTGTCTGGCC TCACAGCACT

